



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/629,329
Source: CIPR
Date Processed by STIC: 8-18-03

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FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

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Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 04/24/2003



OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/629,329

DATE: 08/18/2003

TIME: 09:10:27

Input Set : E:\Utsc761.app
 Output Set: N:\CRF4\08182003\J629329.raw

3 <110> APPLICANT: DARNAY, BRYANT G.
 5 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS USING POLYNUCLEOTIDES AND
 6 POLYPEPTIDES OF RANK-ASSOCIATED INHIBITOR (RAIN)
 8 <130> FILE REFERENCE: UTSC:761US

C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/629,329

11 <141> CURRENT FILING DATE: 2003-07-29
 13 <150> PRIOR APPLICATION NUMBER: 60/399,205
 14 <151> PRIOR FILING DATE: 2002-07-29
 16 <160> NUMBER OF SEQ ID NOS: 23
 18 <170> SOFTWARE: PatentIn Ver. 2.1
 20 <210> SEQ ID NO: 1
 21 <211> LENGTH: 729
 22 <212> TYPE: DNA
 23 <213> ORGANISM: Homo sapiens
 25 <220> FEATURE:
 26 <221> NAME/KEY: CDS
 27 <222> LOCATION: (1)..(729)
 29 <400> SEQUENCE: 1

**Does Not Comply
Corrected Diskette Needed**

PP.5-6

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31	Met Ser Gly Cys Asp Ala Gly Glu Gly Asp Cys Cys Ser Arg Arg Cys	
32	1 5 10 15	
34	ggc gcg cag gac aag gag cat cca aga tac ctg atc cca gaa ctt tgc	96
35	Gly Ala Gln Asp Lys Glu His Pro Arg Tyr Leu Ile Pro Glu Leu Cys	
36	20 25 30	
38	aaa cag ttt tac cat tta ggc tgg gtc act ggg act gga gga gga att	144
39	Lys Gln Phe Tyr His Leu Gly Trp Val Thr Gly Thr Gly Gly Ile	
40	35 40 45	
42	agc ttg aag cat ggc gat gaa atc tac att gct cct tca gga gtg caa	192
43	Ser Leu Lys His Gly Asp Glu Ile Tyr Ile Ala Pro Ser Gly Val Gln	
44	50 55 60	
46	aag gaa cga att cag cct gaa gac atg ttt gtt tgt gat ata aat gaa	240
47	Lys Glu Arg Ile Gln Pro Glu Asp Met Phe Val Cys Asp Ile Asn Glu	
48	65 70 75 80	
50	aag gac ata agt gga cct tcg cca tcg aag aag cta aaa aaa agc cag	288
51	Lys Asp Ile Ser Gly Pro Ser Pro Ser Lys Lys Leu Lys Lys Ser Gln	
52	85 90 95	
54	tgt act cct ctt ttc atg aat gct tac aca atg aga gga gca ggt gca	336
55	Cys Thr Pro Leu Phe Met Asn Ala Tyr Thr Met Arg Gly Ala Gly Ala	
56	100 105 110	
58	gtg att cat acc cac tct aaa gct gct gtg atg gcc aca ctt ctc ttt	384
59	Val Ile His Thr His Ser Lys Ala Ala Val Met Ala Thr Leu Leu Phe	
60	115 120 125	
62	cca gga cgg gag ttt aaa att aca cat caa gag atg ata aaa gga ata	432

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Input Set : E:\Utsc761.app
Output Set: N:\CREF\08182003\J629329 raw

63 Pro Gly Arg Glu Phe Lys Ile Thr His Gln Glu Met Ile Lys Gly Ile
 64 130 135 140
 66 aag aaa tgt act tcc gga ggg tat tat aga tat gat gat atg tta gtg 480
 67 Lys Lys Cys Thr Ser Gly Gly Tyr Tyr Arg Tyr Asp Asp Met Leu Val
 68 145 150 155 160
 70 gta ccc att att gag aat aca cct gag gag aaa ggc ctc aaa gat aga
 71 Val Pro Ile Ile Glu Asn Thr Pro Glu Glu Lys Gly Leu Lys Asp Arg 528
 72 165 170 175
 74 atg gct cat gca atg aat gaa tac cca gac tcc tgt gca gta ctg gtc
 75 Met Ala His Ala Met Asn Glu Tyr Pro Asp Ser Cys Ala Val Leu Val 576
 76 180 185 190
 78 aga cgt cat gga gta tat gtg tgg ggg gaa aca tgg gag aag gcc aaa 624
 79 Arg Arg His Gly Val Tyr Val Trp Gly Glu Thr Trp Glu Lys Ala Lys
 80 195 200 205
 82 acc atg tgt gag tgt tat gac tat tta ttt gat att gcc gta tca atg 672
 83 Thr Met Cys Glu Cys Tyr Asp Tyr Leu Phe Asp Ile Ala Val Ser Met
 84 210 215 220
 86 aag aaa gta gga ctt gat cct tca cag ctc cca gtt gga gaa aat gga 720
 87 Lys Lys Val Gly Leu Asp Pro Ser Gln Leu Pro Val Gly Glu Asn Gly
 88 225 230 235 240
 90 att gtg taa
 91 Ile Val 729
 94 <210> SEQ ID NO: 2
 95 <211> LENGTH: 242
 96 <212> TYPE: PRT
 97 <213> ORGANISM: Homo sapiens
 99 <400> SEQUENCE: 2
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 101 1 5 10 15
 102 Gly Ala Gln Asp Lys Glu His Pro Arg Tyr Leu Ile Pro Glu Leu Cys
 103 20 25 30
 104 Lys Gln Phe Tyr His Leu Gly Trp Val Thr Gly Thr Gly Gly Ile
 105 35 40 45
 106 Ser Leu Lys His Gly Asp Glu Ile Tyr Ile Ala Pro Ser Gly Val Gln
 107 50 55 60
 108 Lys Glu Arg Ile Gln Pro Glu Asp Met Phe Val Cys Asp Ile Asn Glu
 109 65 70 75 80
 110 Lys Asp Ile Ser Gly Pro Ser Pro Ser Lys Lys Leu Lys Lys Ser Gln
 111 85 90 95
 112 Cys Thr Pro Leu Phe Met Asn Ala Tyr Thr Met Arg Gly Ala Gly Ala
 113 100 105 110
 114 Val Ile His Thr His Ser Lys Ala Ala Val Met Ala Thr Leu Leu Phe
 115 115 120 125
 116 Pro Gly Arg Glu Phe Lys Ile Thr His Gln Glu Met Ile Lys Gly Ile
 117 130 135 140
 118 Lys Lys Cys Thr Ser Gly Gly Tyr Tyr Arg Tyr Asp Asp Met Leu Val
 119 145 150 155 160
 120 Val Pro Ile Ile Glu Asn Thr Pro Glu Glu Lys Gly Leu Lys Asp Arg
 121 165 170 175

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Input Set : E:\Utsc761.app
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122 Met Ala His Ala Met Asn Glu Tyr Pro Asp Ser Cys Ala Val Leu Val
123 180 185 190
124 Arg Arg His Gly Val Tyr Val Trp Gly Glu Thr Trp Glu Lys Ala Lys
125 195 200 205
126 Thr Met Cys Glu Cys Tyr Asp Tyr Leu Phe Asp Ile Ala Val Ser Met
127 210 215 220
128 Lys Lys Val Gly Leu Asp Pro Ser Gln Leu Pro Val Gly Glu Asn Gly
129 225 230 235 240
130 Ile Val
134 <210> SEQ ID NO: 3
135 <211> LENGTH: 726
136 <212> TYPE: DNA
137 <213> ORGANISM: Mus musculus
139 <220> FEATURE:
140 <221> NAME/KEY: CDS
141 <222> LOCATION: (1)..(726)
143 <400> SEQUENCE: 3
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146 1 5 10 15
148 gcg cag gac aag gag cac ccc cga ttc ctg atc cca gaa ctt tgc aaa 96
149 Ala Gln Asp Lys Glu His Pro Arg Phe Leu Ile Pro Glu Leu Cys Lys
150 20 25 30
152 cag ttt tac cat ctg ggc tgg gtc acc ggc act gga ggg gga atc agc 144
153 Gln Phe Tyr His Leu Gly Trp Val Thr Gly Thr Gly Gly Ile Ser
154 35 40 45
156 ttg aag cat ggc aat gaa atc tac att gct ccc tca ggc gtg caa aag 192
157 Leu Lys His Gly Asn Glu Ile Tyr Ile Ala Pro Ser Gly Val Gln Lys
158 50 55 60
160 gaa cgc att cag cca gaa gac atg ttt gtg tgt gac att aat gag cag 240
161 Glu Arg Ile Gln Pro Glu Asp Met Phe Val Cys Asp Ile Asn Glu Gln
162 65 70 75 80
164 gac ata agc ggg cct cca gca tct aag aag ctg aaa aaa agc cag tgc 288
165 Asp Ile Ser Gly Pro Pro Ala Ser Lys Lys Leu Lys Lys Ser Gln Cys
166 85 90 95
168 act cct ctt ttc atg aat gct tat acc atg aga gga gct ggc gca gtg 336
169 Thr Pro Leu Phe Met Asn Ala Tyr Thr Met Arg Gly Ala Gly Ala Val
170 100 105 110
172 att cat acc cac tct aaa gct gct gtg atg gct acc ctt ctg ttt cca 384
173 Ile His Thr His Ser Lys Ala Ala Val Met Ala Thr Leu Leu Phe Pro
174 115 120 125
176 gga cag gag ttt aaa att aca cat caa gag atg atc aaa gga ata agg 432
177 Gly Gln Glu Phe Lys Ile Thr His Gln Glu Met Ile Lys Gly Ile Arg
178 130 135 140
180 aaa tgt acc tca gga ggc tat tac aga tac gat gat atg tta gtg gta 480
181 Lys Cys Thr Ser Gly Gly Tyr Tyr Arg Tyr Asp Asp Met Leu Val Val
182 145 150 155 160
184 cct att att gag aac act cct gaa gag aag gat ctc aaa gaa agg atg 528
185 Pro Ile Ile Glu Asn Thr Pro Glu Glu Lys Asp Leu Lys Glu Arg Met

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186	165	170	175	
188	gct cat gcc atg aac gag tac cca gac tcc tgt gcg gtt ctt gtc cg	576		
189	Ala His Ala Met Asn Glu Tyr Pro Asp Ser Cys Ala Val Leu Val Arg			
190	180	185	190	
192	cgt cat ggg gtg tac gtg tgg gga gaa aca tgg gag aaa gca aaa acc	624		
193	Arg His Gly Val Tyr Val Trp Gly Glu Thr Trp Glu Lys Ala Lys Thr			
194	195	200	205	
196	atg tgt gag tgt tat gac tac ctg ttt gac att gct gtc tcc atg aag	672		
197	Met Cys Glu Cys Tyr Asp Tyr Leu Phe Asp Ile Ala Val Ser Met Lys			
198	210	215	220	
200	aag atg gga ctc gat cca aca cag ctc cca gtt gga gaa aat gga att	720		
201	Lys Met Gly Leu Asp Pro Thr Gln Leu Pro Val Gly Glu Asn Gly Ile			
202	225	230	235	240
204	gtg taa			726
205	Val			
208	<210> SEQ ID NO: 4			
209	<211> LENGTH: 241			
210	<212> TYPE: PRT			
211	<213> ORGANISM: Mus musculus			
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216	Ala Gln Asp Lys Glu His Pro Arg Phe Leu Ile Pro Glu Leu Cys Lys			
217	20	25	30	
218	Gln Phe Tyr His Leu Gly Trp Val Thr Gly Thr Gly Gly Ile Ser			
219	35	40	45	
220	Leu Lys His Gly Asn Glu Ile Tyr Ile Ala Pro Ser Gly Val Gln Lys			
221	50	55	60	
222	Glu Arg Ile Gln Pro Glu Asp Met Phe Val Cys Asp Ile Asn Glu Gln			
223	65	70	75	80
224	Asp Ile Ser Gly Pro Pro Ala Ser Lys Lys Leu Lys Lys Ser Gln Cys			
225	85	90	95	
226	Thr Pro Leu Phe Met Asn Ala Tyr Thr Met Arg Gly Ala Gly Ala Val			
227	100	105	110	
228	Ile His Thr His Ser Lys Ala Ala Val Met Ala Thr Leu Leu Phe Pro			
229	115	120	125	
230	Gly Gln Glu Phe Lys Ile Thr His Gln Glu Met Ile Lys Gly Ile Arg			
231	130	135	140	
232	Lys Cys Thr Ser Gly Gly Tyr Tyr Arg Tyr Asp Asp Met Leu Val Val			
233	145	150	155	160
234	Pro Ile Ile Glu Asn Thr Pro Glu Glu Lys Asp Leu Lys Glu Arg Met			
235	165	170	175	
236	Ala His Ala Met Asn Glu Tyr Pro Asp Ser Cys Ala Val Leu Val Arg			
237	180	185	190	
238	Arg His Gly Val Tyr Val Trp Gly Glu Thr Trp Glu Lys Ala Lys Thr			
239	195	200	205	
240	Met Cys Glu Cys Tyr Asp Tyr Leu Phe Asp Ile Ala Val Ser Met Lys			
241	210	215	220	
242	Lys Met Gly Leu Asp Pro Thr Gln Leu Pro Val Gly Glu Asn Gly Ile			

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Use of <220> Feature(NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec. 1 823 of new Rules)

Seq#:5

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/629,329

DATE: 08/18/2003

TIME: 09:10:28

Input Set : E:\Utsc761.app

Output Set: N:\CRF4\08182003\J629329.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number
L:253 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:5, <213>

ORGANISM:Artificial Sequence

L:253 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:5, <213>

ORGANISM:Artificial Sequence

L:253 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:253